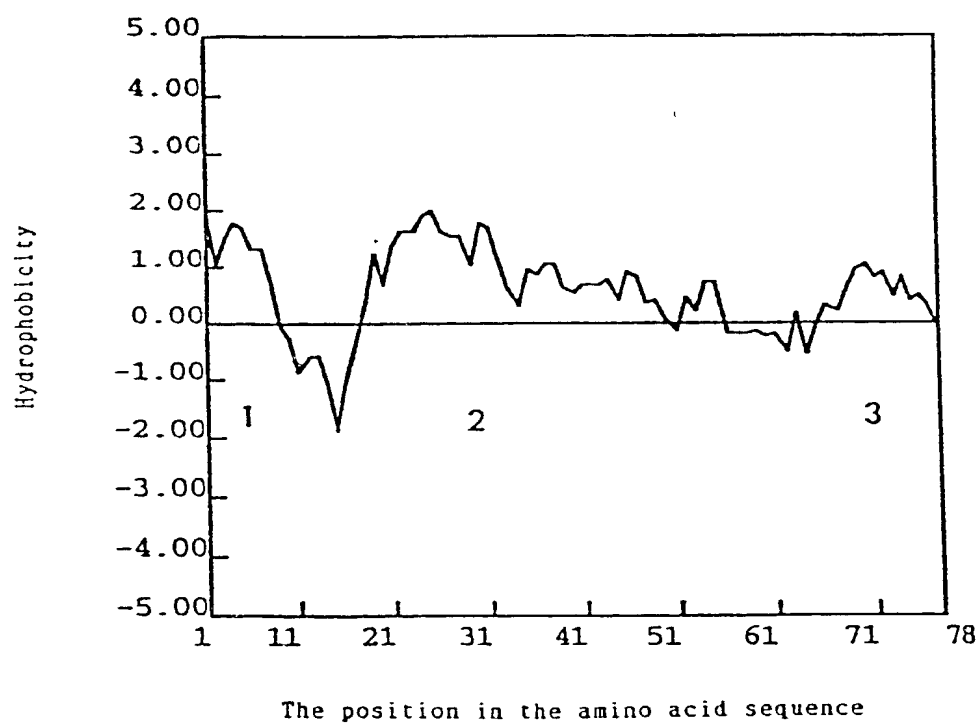


1/19

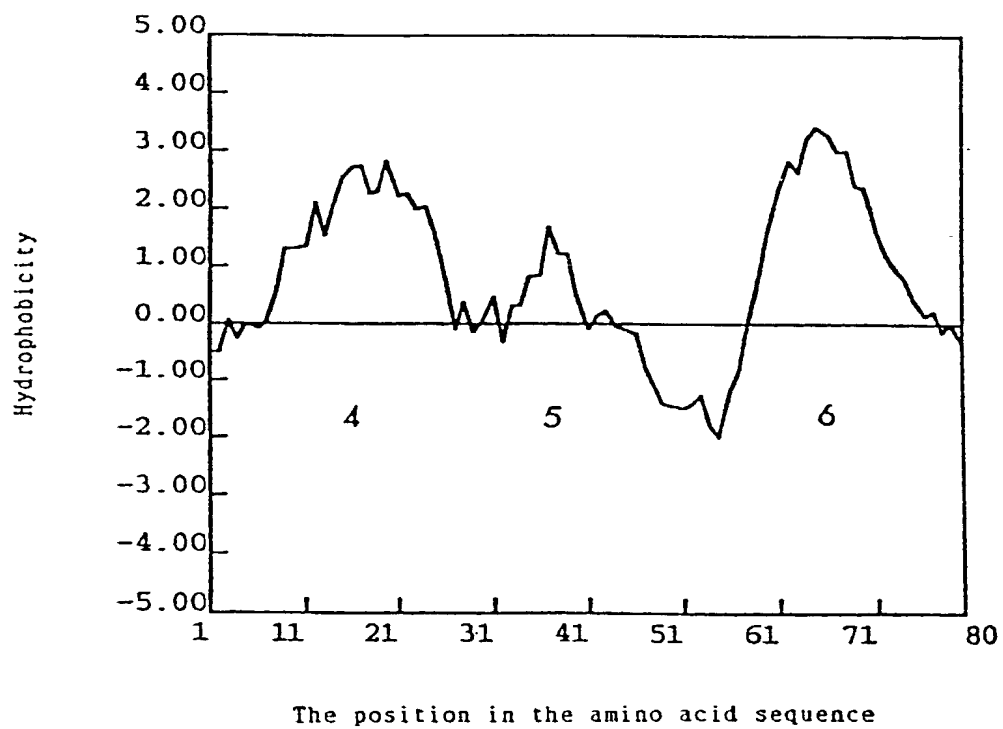
5'		10		19		28		37		46		55						
	GTG	GCC	ATG	CTG	GCC	AAC	GCC	CTG	GTC	TGT	CAT	GTC	ATC	TTC	AAG	AAC	CAG	CGA
									Val	Cys	His	Val	Ile	Phe	Lys	Asn	Gln	Arg
		64		73		82		91		100		109						
	ATG	CAC	TCG	GCC	ACC	AGC	CTC	TTC	ATC	GTC	AAC	CTG	GCA	GTT	GCC	GAC	ATA	ATG
	Met	His	Ser	Ala	Thr	Ser	Leu	Phe	Ile	Val	Asn	Leu	Ala	Val	Ala	Asp	Ile	Met
		118		127		136		145		154		163						
	ATC	ACG	CTG	CTC	AAC	ACC	CCC	TTC	ACT	TTG	GTT	CGC	TTT	GTC	AAC	AGC	ACA	TGG
	Ile	Thr	Leu	Leu	Asn	Thr	Pro	Phe	Thr	Leu	Val	Arg	Phe	Val	Asn	Ser	Thr	Trp
		172		181		190		199		208		217						
	ATA	TTT	GGG	AAG	GCC	ATG	TOC	CAT	GTC	AGC	CGC	TTT	GCC	CAG	TAC	TGC	TCA	CTG
	Ile	Phe	Gly	Lys	Gly	Met	Cys	His	Val	Ser	Arg	Phe	Ala	Gln	Tyr	Cys	Ser	Leu
		226		235														
	CAC	GTC	TCA	GCA	CTG	ACA	3'											
	His	Val	Ser	Ala	Leu	Thr												

5'	9			18			27			36			45			54		
	GAG	CCA	GCT	GAC	CTC	TTC	TGG	AAG	AAC	CTG	GAC	TTG	CCC	ACC	TTC	ATC	CTG	CTC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Glu	Pro	Ala	Asp	Leu	Phe	Trp	Lys	Asn	Leu	Asp	Leu	Pro	Thr	Phe	Ile	Leu	Leu
	63			72			81			90			99			108		
	AAC	ATC	CTG	CCC	CTC	CTC	ATC	ATC	TCT	GTG	GCC	TAC	GTT	CGT	GTG	ACC	AAG	AAA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Asn	Ile	Leu	Pro	Leu	Leu	Ile	Ile	Ser	Val	Ala	Tyr	Val	Arg	Val	Thr	Lys	Lys
	117			126			135			144			153			162		
	CTG	TGG	CTG	TGT	AAT	ATG	ATT	GTC	GAT	GTG	ACC	ACA	GAG	CAG	TAC	TTT	GCC	CTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Trp	Leu	Cys	Asn	Met	Ile	Val	Asp	Val	Thr	Thr	Glu	Gln	Tyr	Phe	Ala	Leu
	171			180			189			198			207			216		
	CGG	CCC	AAA	AAG	AAG	AAG	ACC	ATC	AAG	ATG	TTG	ATG	CTG	GTC	GTA	GTC	CTC	TTT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Arg	Pro	Lys	Lys	Lys	Lys	Thr	Ile	Lys	Met	Leu	Met	Leu	Val	Val	Val	Leu	Phe
	225			234														
	GCC	CTC	TGC	TGG	TTG	CCT	CTC	GAC	3'									
	---	---	---	---	---	---	---	---	---									
	Ala	Leu	Cys	Trp	Leu	Pro	Leu	Asp										

3/19



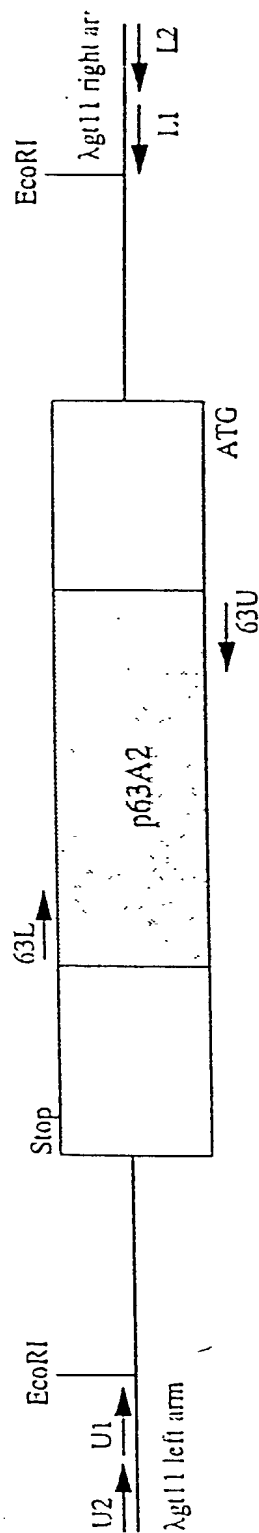
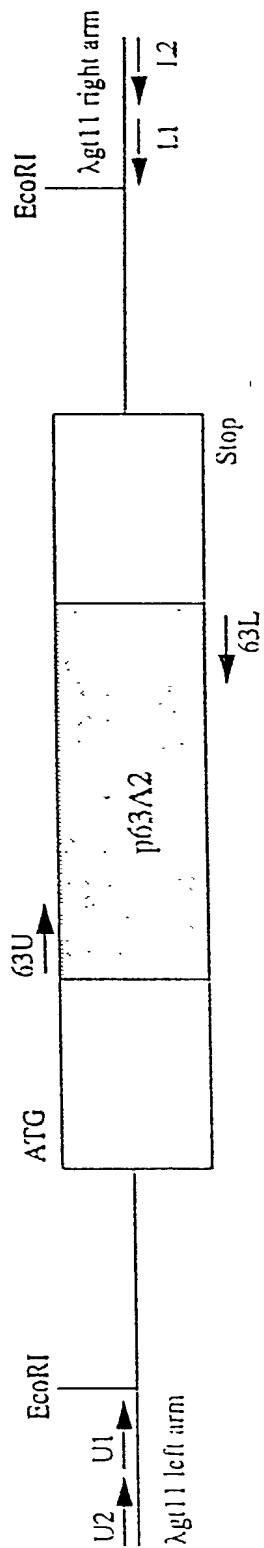
4/19



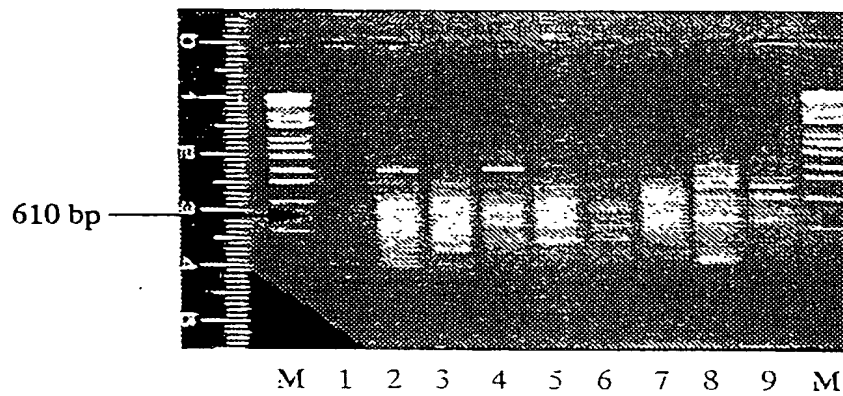
5/19

p63A2	1	10	20	30	40	50	
P30731	1	VCHVLEKQOR	MHSATSLFIV	NLAVADIMIT	LLNTPFTLVR	EVNSTWIEFGK	50
	1	VCHVLEKQOR	MHSATSLFIV	NLAVADIMIT	LLNTPFTLVR	EVNSTWIEFGK	50
p63A2	51	60	70	80	90	100	
P30731	51	GMCHVSRFQ	YCSLHVSALT	LTALAVIDRHQ	VIMHPLKPRI	SITKGVITYLA	100
	51	GMCHVSRFQ	YCSLHVSALT	LTALAVIDRHQ	VIMHPLKPRI	SITKGVITYLA	100
p63A2	101	110	120	130	140	150	
P30731	101	VIWVMATFFS	LPHAICQKLF	TFKYSEDIVR	SICLPDPFPH	ADLEWKNLDL	150
	101	VIWVMATFFS	LPHAICQKLF	TFKYSEDIVR	SICLPDPFPH	ADLEWKNLDL	150
p63A2	151	160	170	180	190	200	
P30731	151	PTFILLNIEP	LLITSVAYVR	VTKKLWLCNM	IVDVTEQYF	ALRPKGGKTI	200
	151	PTFILLNIEP	LLITSVAYVR	VTKKLWLCNM	IVDVTEQYF	ALRPKGGKTI	200
p63A2	201	210	220	230	240	250	
P30731	201	KHMLVWVL	.....	.....	.....	.....	250
	201	KHMLVWVL	.....	.....	.....	.....	250

6/19



7/19



M:  $\lambda$ DNA/Sty I marker

lane 1; 63U~63L

lane 2: U1~63U

lane 3; U1~63L

lane 4: U2~63U

lane 5; U2~63L

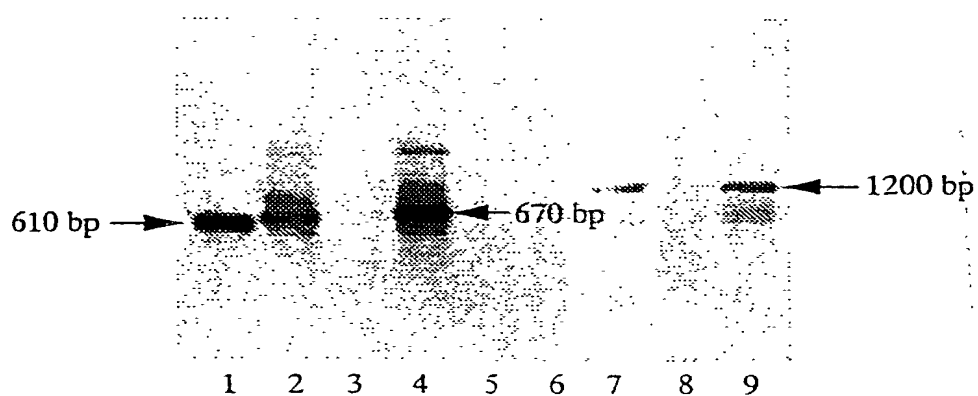
lane 6: L1~63U

lane 7: L1~63L

lane 8; L2~63U

lane 9; L2~63L

8/19

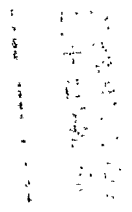


lane 1 ; 63U~63L  
lane 2 ; U1~63U  
lane 3 ; U1~63L  
lane 4 ; U2~63U  
lane 5 ; U2~63L  
lane 6 ; L1~63U  
lane 7 ; L1~63L  
lane 8 ; L2~63U  
lane 9 ; L2~63L

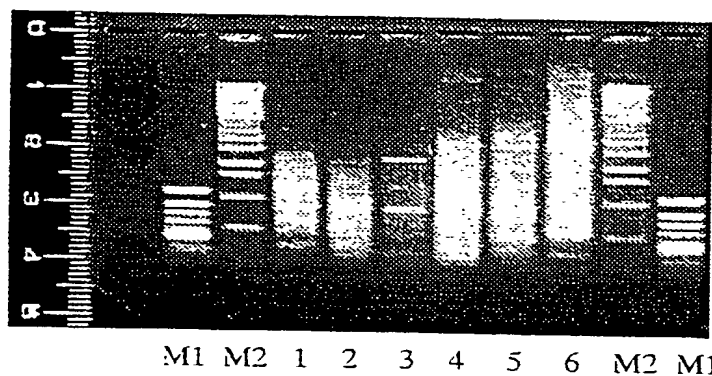


63A2-5'. SEQ 10 20 30 40 50  
GGGCCCCCTTACACCTTTGTGATTGATCCGGGGTTTC-AAGGGTGCATGATGAG  
MUSGIR.DNA  
GGGCTTCCTCTGTGCCCCCGTCCCTGCTCCCAAGGCTCCCTCTGTGGTGTGACTCCTC  
130 140 150 160 170 180  
60 70 80 90 100 110  
63A2-5'. SEQ GAGTAAAGCCACATGAGCAGGGCTTCAACCGTGGGTTCTGGGACTCAAGCCCTAAGC  
MUSGIR.DNA  
TAGCCCGGTGCGCTCAGC--CCCTGCAC-CAGCCTCCAGGCACAGAGCCCGCAGGGA  
190 200 210 220 230 240  
120 130 140 150 160 170  
63A2-5'. SEQ TTCCTGCCACAAAGTTCTCCCAAGGAGGGGTGGCTCCTGCATAATGTCCTCAACCTC  
MUSGIR.DNA  
GCTCAGGCC-----TTGTGCTTAGAGCTGCAAGTGGCT-GGACATGAAGTTCTCTCTGTC  
250 260 270 280 290  
180 190 200 210 220 230  
63A2-5'. SEQ TTGCTGCTCTGTCTCTCTCCCTTGGTGGAGCCACCGAGGCCACGAGGGCCGGCCGAC  
MUSGIR.DNA  
CTGCTTCTCTTCTCTCTCTGCTCAGTGGAGCTACTGAGCAACCGCAGGTGCTCACTGAG  
300 310 320 330 340 350  
240 250 260 270 280 290  
63A2-5'. SEQ GAGCAGAGCGCGGAGGGCCCTGGCCATGCCAAATGCCCTGCACCTTCTCTTGAAC  
MUSGIR.DNA  
CATCCAGCATGAGGAGCGCCCTGACCGGGCCCAACGCCCTCTCGCACTTC--TGGGCC  
360 370 380 390 400 410  
300 310 320 330 340 350  
63A2-5'. SEQ AACTACACCTTCTCGCACTGGCAGAACTTTGTGGCAGAGGTGCTACGCGCGCTGAGTCC  
MUSGIR.DNA  
AACTACACTTCTCTGACTGGCAGAACTTCGTGGCAGGAGAGCTTATGGGGCCGAGTCC  
420 430 440 450 460 470  
360 370 380  
63A2-5'. SEQ CAGAACCCACAGGTGAAAGCCCTGCTC  
MUSGIR.DNA  
CAGAACCCACAGGTGAAAGCACTGCTC  
480 490 500

10/19



12/19



M1 ;  $\phi$ X174 / HincII

M2 ;  $\lambda$  / StyI

lane 1 ; 63U ~ Anchor Primer

lane 2 ; 63-6 ~ Anchor Primer

lane 3 ; 63-7 ~ Anchor Primer

lane 4 ; 63-6 ~ Anchor Primer

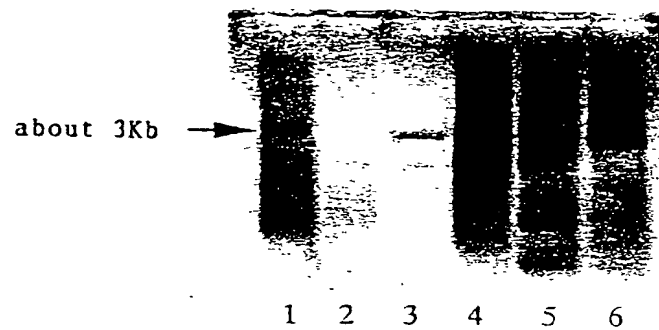
lane 5 ; 63-7 ~ Anchor Primer

lane 6 ; 63-8 ~ Anchor Primer

Primary PCR

Secondary PCR

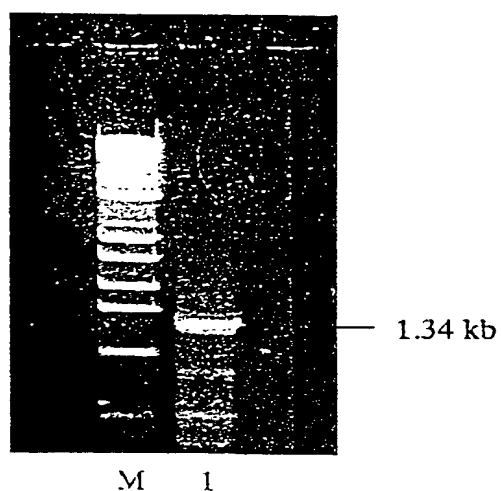
13/19



lane 1 ; 63U~Anchor Primer	Primary PCR
lane 2 ; 63-6~Anchor Primer	
lane 3 ; 63-7~Anchor Primer	
lane 4 ; 63-6~Anchor Primer	Secondary PCR
lane 5 ; 63-7~Anchor Primer	
lane 6 ; 63-8~Anchor Primer	



15/19



M ;  $\lambda$  / StyI  
lane 1 ; Whole Brain

16/19

5' ATG GTC CCT CAC CTC TTG CTG CTC TGT CTC CTC CCC TTG GTG CGA GCC ACC GAG  
Met Val Pro His Leu Leu Leu Leu Cys Leu Leu Pro Leu Val Arg Ala Thr Glu

CCC CAC GAG GGC CGG GCC GAC GAG CAG AGC GCG GAG GCG GCC CTG GCC GTG CCC  
Pro His Glu Gly Arg Ala Asp Glu Gln Ser Ala Glu Ala Ala Leu Ala Val Pro

AAT GCC TCG CAC TTC TTC TCT TGG AAC AAC TAC ACC TTC TCC GAC TGG CAG AAC  
Asn Ala Ser His Phe Phe Ser Trp Asn Asn Tyr Thr Phe Ser Asp Trp Gln Asn

TTT GTG GGC AGG AGG CGC TAC GGC GCT GAG TCC CAG AAC CCC ACG GTG AAA GCC  
Phe Val Gly Arg Arg Arg Tyr Gly Ala Glu Ser Gln Asn Pro Thr Val Lys Ala

CTG CTC ATT GTG GCT TAC TCC TTC ATC ATT GTC TTC TCA CTC TTT GGC AAC GTC  
Leu Leu Ile Val Ala Tyr Ser Phe Ile Ile Val Phe Ser Leu Phe Gly Asn Val

CTG GTC TGT CAT GTC ATC TTC AAG AAC CAG CGA ATG CAC TCG GCC ACC AGC CTC  
Leu Val Cys His Val Ile Phe Lys Asn Gln Arg Met His Ser Ala Thr Ser Leu

TTC ATC GTC AAC CTG GCA GTT GCC GAC ATA ATG ATC ACG CTG CTC AAC ACC CCC  
Phe Ile Val Asn Leu Ala Val Ala Asp Ile Met Ile Thr Leu Leu Asn Thr Pro

TTC ACT TTG GTT CGC TTT GTG AAC AGC ACA TGG ATA TTT GGG AAG GGC ATG TGC  
Phe Thr Leu Val Arg Phe Val Asn Ser Thr Trp Ile Phe Gly Lys Gly Met Cys

CAT GTC AGC CGC TTT GCC CAG TAC TGC TCA CTG CAC GTC TCA GCA CTG ACA CTG  
His Val Ser Arg Phe Ala Gln Tyr Cys Ser Leu His Val Ser Ala Leu Thr Leu

ACA GCC ATT GCG GTG GAT CGC CAC CAG GTC ATC ATG CAC CCC TTG AAA CCC CGG  
Thr Ala Ile Ala Val Asp Arg His Gln Val Ile Met His Pro Leu Lys Pro Arg

ATC TCA ATC ACA AAG GGT GTC ATC TAC ATC GCT GTC ATC TGG ACC ATG GCT ACG  
Ile Ser Ile Thr Lys Gly Val Ile Tyr Ile Ala Val Ile Trp Thr Met Ala Thr

TTC TTT TCA CTC CCA CAT GCT ATC TGC CAG AAA TTA TTT ACC TTC AAA TAC AGT  
Phe Phe Ser Leu Pro His Ala Ile Cys Gln Lys Leu Phe Thr Phe Lys Tyr Ser

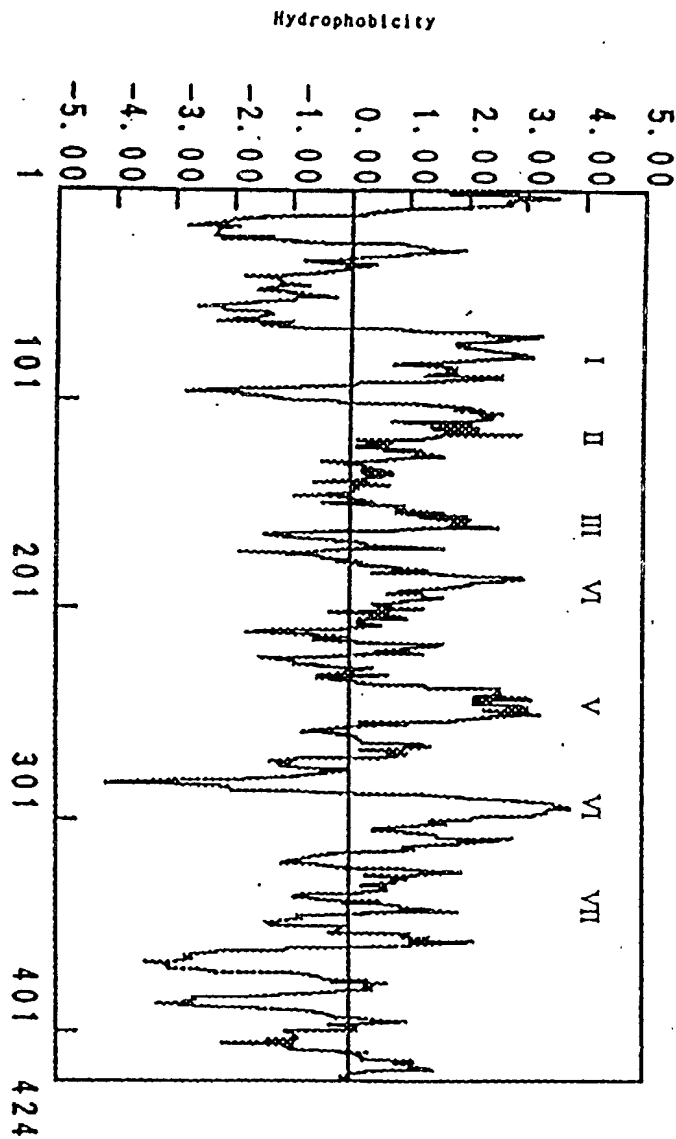
GAG GAC ATT GTG CGC TCC CTC TGC CTG CCA GAC TTC CCT GAG CCA GCT GAC CTC  
Glu Asp Ile Val Arg Ser Leu Cys Leu Pro Asp Phe Pro Glu Pro Ala Asp Leu



17/19

711	720	729	738	747	756
TTC TGG AAG TAC CTG GAC TTG GCC ACC TTC ATC CTG CTC TAC ATC CTG CCC CTC					
Phe Trp Lys Tyr Leu Asp Leu Ala Thr Phe Ile Leu Leu Tyr Ile Leu Pro Leu					
765	774	783	792	801	810
CTC ATC ATC TCT GTG GCC TAC GCT CGT GTG GCC AAG AAA CTG TGG CTG TGT AAT					
Leu Ile Ile Ser Val Ala Tyr Ala Arg Val Ala Lys Lys Leu Trp Leu Cys Asn					
819	828	837	846	855	864
ATG ATT GGC GAT GTG ACC ACA GAG CAG TAC TTT GCC CTG CGG CGC AAA AAG AAG					
Met Ile Gly Asp Val Thr Thr Glu Gln Tyr Phe Ala Leu Arg Arg Lys Lys Lys					
873	882	891	900	909	918
AAG ACC ATC AAG ATG TTG ATG CTG GTG GTA GTC CTC TTT GCC CTC TGC TGG TTC					
Lys Thr Ile Lys Met Leu Met Leu Val Val Val Leu Phe Ala Leu Cys Trp Phe					
927	936	945	954	963	972
CCC CTC AAC TGC TAC GTC CTC CTC CTG TCC AGC AAG GTC ATC CGC ACC AAC AAT					
Pro Leu Asn Cys Tyr Val Leu Leu Leu Ser Ser Lys Val Ile Arg Thr Asn Asn					
981	990	999	1008	1017	1026
GCC CTC TAC TTT GCC TTC CAC TGG TTT GCC ATG AGC AGC ACC TGC TAT AAC CCC					
Ala Leu Tyr Phe Ala Phe His Trp Phe Ala Met Ser Ser Thr Cys Tyr Asn Pro					
1035	1044	1053	1062	1071	1080
TTC ATA TAC TGC TGG CTG AAC GAG AAC TTC AGG ATT GAG CTA AAG GCA TTA CTG					
Phe Ile Tyr Cys Trp Leu Asn Glu Asn Phe Arg Ile Glu Leu Lys Ala Leu Leu					
1089	1098	1107	1116	1125	1134
AGC ATG TGT CAA AGA CCT CCC AAG CCT CAG GAG GAC AGG CCA CCC TCC CCA GTT					
Ser Met Cys Gln Arg Pro Pro Lys Pro Gln Glu Asp Arg Pro Pro Ser Pro Val					
1143	1152	1161	1170	1179	1188
CCT TCC TTC AGG GTG GCC TGG ACA GAG AAG AAT GAT GGC CAG AGG GCT CCC CTT					
Pro Ser Phe Arg Val Ala Trp Thr Glu Lys Asn Asp Gly Gln Arg Ala Pro Leu					
1197	1206	1215	1224	1233	1242
GCC AAT AAC CTC CTG CCC ACC TCC CAA CTC CAG TCT GGG AAG ACA GAC CTG TCA					
Ala Asn Asn Leu Leu Pro Thr Ser Gln Leu Gln Ser Gly Lys Thr Asp Leu Ser					
1251	1260	1269			
TCT GTG GAA CCC ATT GTG ACG ATG AGT TAG 3'					
Ser Val Glu Pro Ile Val Thr Met Ser ***					

18/19



63A2. AMI MUSGIR. AMI	1 1	10 10	20 20	30 30	40 40	50 50
	1 1	10 10	20 20	30 30	40 40	50 50
	1 1	10 10	20 20	30 30	40 40	50 50
63A2. AMI MUSGIR. AMI	51 51	60 60	70 70	80 80	90 90	100 100
	51 51	60 60	70 70	80 80	90 90	100 100
63A2. AMI MUSGIR. AMI	101 101	110 110	120 120	130 130	140 140	150 150
	101 101	110 110	120 120	130 130	140 140	150 150
63A2. AMI MUSGIR. AMI	151 151	160 160	170 170	180 180	190 190	200 200
	151 151	160 160	170 170	180 180	190 190	200 200
63A2. AMI MUSGIR. AMI	201 201	210 210	220 220	230 230	240 240	250 250
	201 201	210 210	220 220	230 230	240 240	250 250
63A2. AMI MUSGIR. AMI	251 251	260 260	270 270	280 280	290 290	300 300
	251 251	260 260	270 270	280 280	290 290	300 300
63A2. AMI MUSGIR. AMI	301 301	310 310	320 320	330 330	340 340	350 350
	301 301	310 310	320 320	330 330	340 340	350 350
63A2. AMI MUSGIR. AMI	351 351	360 360	370 370	380 380	390 390	400 400
	351 351	360 360	370 370	380 380	390 390	400 400
63A2. AMI MUSGIR. AMI	401 401	410 410	420 420	430 430	440 440	450 450
	401 401	410 410	420 420	430 430	440 440	450 450